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1600

RAW SEQUENCE LISTING

DATE: 07/03/2003

PATENT APPLICATION: US/09/534,861C

TIME: 15:29:31

Input Set : A:\ARNO115313.txt

Output Set: N:\CRF4\07032003\I534861C.raw

3 <110> APPLICANT: Smeekens, J.C.M.
4 Ebskamp, Michael
5 Geerts, Hendrikis
6 Weisbeek, Petrus
8 <120> TITLE OF INVENTION: PRODUCTION OF OLIGOSACCHARIDES IN TRANSGENIC PLANTS
10 <130> FILE REFERENCE: ARNO-1-15313
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/534,861C
13 <141> CURRENT FILING DATE: 2000-03-24
15 <150> PRIOR APPLICATION NUMBER: US 09/019,385
16 <151> PRIOR FILING DATE: 1998-02-05
18 <150> PRIOR APPLICATION NUMBER: US 09/193,385
19 <151> PRIOR FILING DATE: 1998-11-17
21 <150> PRIOR APPLICATION NUMBER: US 08/479,470
22 <151> PRIOR FILING DATE: 1995-06-07
24 <150> PRIOR APPLICATION NUMBER: NL 1000064
25 <151> PRIOR FILING DATE: 1995-04-05
27 <150> PRIOR APPLICATION NUMBER: NL 9401140
28 <151> PRIOR FILING DATE: 1994-08-07
30 <160> NUMBER OF SEQ ID NOS: 12
32 <170> SOFTWARE: PatentIn version 3.2
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 2094
36 <212> TYPE: DNA
37 <213> ORGANISM: Barley
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (46)..(1923)
44 <400> SEQUENCE: 1
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46 Met Gly Ser His
47 1
49 ggc aag cca ccg cta ccg tac gcc tac aag ccg ctg ccc tcg gac gcc 105
50 Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu Pro Ser Asp Ala
51 5 10 15 20
53 gcc gac ggt aag ccg acc gcc tgc atg agg tgg tcc gcg tgt gcc acc 153
54 Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser Ala Cys Ala Thr
55 25 30 35
57 gtg ctg acg gcc tcg gcc atg gcg gtg gtg gtg gtc ggc gcc acg ctc 201
58 Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val Gly Ala Thr Leu
59 40 45 50
61 ctg gcg gga ttg agg atg gag cag gcc gtc gac gag gag gcg gcg gcg 249
62 Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu Glu Ala Ala Ala
63 55 60 65

p.b

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65	ggc ggg ttc ccg tgg agc aac gag atg ctg cag tgg cag cgc agc ggt	297
66	Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ser Gly	
67	70 75 80	
69	tac cat ttc cag acg gcc aag aac tac atg agc gat ccc aac ggc ctg	345
70	Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp Pro Asn Gly Leu	
71	85 90 95 100	
73	atg tat tac cgt gga tgg tac cac atg ttc tac cag tac aac ccg gtg	393
74	Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln Tyr Asn Pro Val	
75	105 110 115	
77	ggc acc gac tgg gac gac ggc atg gag tgg ggc cac gcc gtg tcc cgg	441
78	Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His Ala Val Ser Arg	
79	120 125 130	
81	aac ctt gtc caa tgg cgc acc ctc cct atc gcc atg gtg gcc gac cag	489
82	Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met Val Ala Asp Gln	
83	135 140 145	
85	tgg tac gac atc ctc gga gtc ctc tcg ggc tcc atg acg gtg cta ccc	537
86	Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met Thr Val Leu Pro	
87	150 155 160	
89	aac ggg acg gtc atc atg atc tac acg ggc gcc acc aac gcc tcc gcc	585
90	Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr Asn Ala Ser Ala	
91	165 170 175 180	
93	gtg gag gtc cag tgc atc gcc acc ccg gcc gac ccc aac gac ccc ctc	633
94	Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro Asn Asp Pro Leu	
95	185 190 195	
97	ctc cgc ccg tgg acc aag cac ccc gcc aac ccc gtc atc tgg tcg ccg	681
98	Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val Ile Trp Ser Pro	
99	200 205 210	
101	ccg ggg gtc ggc acc aag gat ttc cga gac ccg atg acc gcc tgg tac	729
102	Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met Thr Ala Trp Tyr	
103	215 220 225	
105	gac gag tcc gac gag aca tgg cgc acc ctc ctc ggg tcc aag gac gac	777
106	Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly Ser Lys Asp Asp	
107	230 235 240	
109	cac gac ggc cac cac gac ggc atc gcc atg atg tac aag acc aag gac	825
110	His Asp Gly His His Asp Gly Ile Ala Met Met Tyr Lys Thr Lys Asp	
111	245 250 255 260	
113	ttc ctc aac tac gag ctc atc ccg ggc atc ttg cac ccg gtg gtg cgc	873
114	Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His Arg Val Val Arg	
115	265 270 275	
117	acc ggc gag tgg gag tgc atc gac ttc tac ccc gtc ggc ccg aga agc	921
118	Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val Gly Arg Arg Ser	
119	280 285 290	
121	agc gac aac tcg tcg gag atg ctg cac gtg ttg aag gcg agc atg gac	969
122	Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys Ala Ser Met Asp	
123	295 300 305	
125	gac gaa ccg cac gac tac tac tcg ctg ggc acg tac gac tcg gcg gcc	1017
126	Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr Asp Ser Ala Ala	
127	310 315 320	
129	aac acg tgg acg ccc atc gac ccg gag ctc gac ttg ggg atc ggg ctg	1065

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130	Asn	Thr	Trp	Thr	Pro	Ile	Asp	Pro	Glu	Leu	Asp	Leu	Gly	Ile	Gly	Leu	
131	325					330					335					340	
133	aga	tac	gac	tgg	gga	aag	ttt	tat	gcg	tcc	acc	tcc	ttc	tat	gat	ccg	1113
134	Arg	Tyr	Asp	Trp	Gly	Lys	Phe	Tyr	Ala	Ser	Thr	Ser	Phe	Tyr	Asp	Pro	
135					345					350					355		
137	gcc	aag	aac	cgg	cgc	gtg	ctc	atg	ggg	tac	gtc	ggc	gag	gtc	gac	tcc	1161
138	Ala	Lys	Asn	Arg	Arg	Val	Leu	Met	Gly	Tyr	Val	Gly	Glu	Val	Asp	Ser	
139				360					365					370			
141	aag	cgg	gct	gat	gtc	gtc	aag	gga	tgg	gct	tcc	att	cag	tca	gtt	cct	1209
142	Lys	Arg	Ala	Asp	Val	Val	Lys	Gly	Trp	Ala	Ser	Ile	Gln	Ser	Val	Pro	
143			375					380					385				
145	agg	acg	gtg	gct	ctg	gat	gag	aag	acc	cgg	acg	aac	ctc	ctg	ctc	tgg	1257
146	Arg	Thr	Val	Ala	Leu	Asp	Glu	Lys	Thr	Arg	Thr	Asn	Leu	Leu	Leu	Trp	
147		390					395					400					
149	ccc	gtt	gag	gag	atc	gag	acc	ctc	cgc	ctc	aat	gcc	acg	gaa	ctg	acc	1305
150	Pro	Val	Glu	Glu	Ile	Glu	Thr	Leu	Arg	Leu	Asn	Ala	Thr	Glu	Leu	Thr	
151	405				410					415					420		
153	gac	gtt	acc	att	aac	act	ggc	tcc	gtc	atc	cat	atc	ccg	ctc	cgc	caa	1353
154	Asp	Val	Thr	Ile	Asn	Thr	Gly	Ser	Val	Ile	His	Ile	Pro	Leu	Arg	Gln	
155				425					430						435		
157	ggc	act	cac	gct	cga	cat	gcg	gag	gcc	tct	ttc	cac	ctt	gat	gct	tcc	1401
158	Gly	Thr	His	Ala	Arg	His	Ala	Glu	Ala	Ser	Phe	His	Leu	Asp	Ala	Ser	
159			440					445					450				
161	gcc	gtg	gct	gcc	ctc	aac	gag	gcc	gat	gtg	ggc	tac	aac	tgc	agt	agc	1449
162	Ala	Val	Ala	Ala	Leu	Asn	Glu	Ala	Asp	Val	Gly	Tyr	Asn	Cys	Ser	Ser	
163			455				460					465					
165	agc	ggc	ggc	gct	gtt	aac	cgc	ggc	gcg	cta	ggc	ccc	ttc	ggc	ctc	ctc	1497
166	Ser	Gly	Gly	Ala	Val	Asn	Arg	Gly	Ala	Leu	Gly	Pro	Phe	Gly	Leu	Leu	
167		470					475					480					
169	gtc	ctc	gcc	gcc	ggt	gac	cgc	cgt	ggc	gag	caa	acg	gcg	gtc	tac	ttc	1545
170	Val	Leu	Ala	Ala	Gly	Asp	Arg	Arg	Gly	Glu	Gln	Thr	Ala	Val	Tyr	Phe	
171	485				490					495					500		
173	tac	gtg	tct	agg	ggc	ctt	gac	gga	ggc	ctc	cac	acc	agc	ttc	tgc	caa	1593
174	Tyr	Val	Ser	Arg	Gly	Leu	Asp	Gly	Gly	Leu	His	Thr	Ser	Phe	Cys	Gln	
175				505					510					515			
177	gat	gag	ctg	aga	tcg	tca	cga	gcc	aag	gat	gtg	acc	aag	cgt	gtc	atc	1641
178	Asp	Glu	Leu	Arg	Ser	Ser	Arg	Ala	Lys	Asp	Val	Thr	Lys	Arg	Val	Ile	
179			520						525				530				
181	ggg	agc	acg	gtg	ccg	gtg	ctc	gac	ggt	gag	gct	ttg	tca	atg	agg	gtg	1689
182	Gly	Ser	Thr	Val	Pro	Val	Leu	Asp	Gly	Glu	Ala	Leu	Ser	Met	Arg	Val	
183			535					540					545				
185	ctc	gtg	gat	cac	tcc	atc	gtg	cag	ggc	ttc	gac	atg	ggc	ggg	agg	acc	1737
186	Leu	Val	Asp	His	Ser	Ile	Val	Gln	Gly	Phe	Asp	Met	Gly	Gly	Arg	Thr	
187		550					555				560						
189	acg	atg	acc	tcg	cgg	gtg	tac	ccg	atg	gag	tcg	tat	cag	gag	gca	aga	1785
190	Thr	Met	Thr	Ser	Arg	Val	Tyr	Pro	Met	Glu	Ser	Tyr	Gln	Glu	Ala	Arg	
191	565				570					575				580			
193	gtc	tac	ttg	ttc	aac	aac	gcc	acc	ggt	gcc	agc	gtg	acg	gcg	gaa	agg	1833
194	Val	Tyr	Leu	Phe	Asn	Asn	Ala	Thr	Gly	Ala	Ser	Val	Thr	Ala	Glu	Arg	

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195          585          590          595
197 ctg gtc gtg cac gag atg gac tcg gca cac aac cag ctc tcc aat gag      1881
198 Leu Val Val His Glu Met Asp Ser Ala His Asn Gln Leu Ser Asn Glu
199          600          605          610
201 gac gat ggc atg tat ctt cat caa gtt ctt gaa tct cgt cat      1923
202 Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser Arg His
203          615          620          625
205 taataagcta cattggatca aagaagatca ccagggaagg gcaattcata cataaatcga      1983
207 atcattctgc acaacctcgc ttgcagcatg cattgaaaca tctgtatttg gatcatcttc      2043
209 ttcatttatg tcatagtga ctatattact ttgtaaaaaa aaaaaaaaaa a      2094
212 <210> SEQ ID NO: 2
213 <211> LENGTH: 626
214 <212> TYPE: PRT
215 <213> ORGANISM: Barley
217 <400> SEQUENCE: 2
219 Met Gly Ser His Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu
220 1          5          10          15
223 Pro Ser Asp Ala Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser
224          20          25          30
227 Ala Cys Ala Thr Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val
228          35          40          45
231 Gly Ala Thr Leu Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu
232          50          55          60
235 Glu Ala Ala Ala Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp
236 65          70          75          80
239 Gln Arg Ser Gly Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp
240          85          90          95
243 Pro Asn Gly Leu Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln
244          100          105          110
247 Tyr Asn Pro Val Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His
248          115          120          125
251 Ala Val Ser Arg Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met
252          130          135          140
255 Val Ala Asp Gln Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met
256 145          150          155          160
259 Thr Val Leu Pro Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr
260          165          170          175
263 Asn Ala Ser Ala Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro
264          180          185          190
267 Asn Asp Pro Leu Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val
268          195          200          205
271 Ile Trp Ser Pro Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met
272          210          215          220
275 Thr Ala Trp Tyr Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly
276 225          230          235          240
279 Ser Lys Asp Asp His Asp Gly His His Asp Gly Ile Ala Met Met Tyr
280          245          250          255
283 Lys Thr Lys Asp Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His
284          260          265          270

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287 Arg Val Val Arg Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val
288          275          280          285
291 Gly Arg Arg Ser Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys
292          290          295          300
295 Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr
296 305          310          315          320
299 Asp Ser Ala Ala Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu
300          325          330          335
303 Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser
304          340          345          350
307 Phe Tyr Asp Pro Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly
308          355          360          365
311 Glu Val Asp Ser Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile
312          370          375          380
315 Gln Ser Val Pro Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn
316 385          390          395          400
319 Leu Leu Leu Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala
320          405          410          415
323 Thr Glu Leu Thr Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile
324          420          425          430
327 Pro Leu Arg Gln Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His
328          435          440          445
331 Leu Asp Ala Ser Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr
332          450          455          460
335 Asn Cys Ser Ser Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro
336 465          470          475          480
339 Phe Gly Leu Leu Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr
340          485          490          495
343 Ala Val Tyr Phe Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr
344          500          505          510
347 Ser Phe Cys Gln Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr
348          515          520          525
351 Lys Arg Val Ile Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu
352          530          535          540
355 Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met
356 545          550          555          560
359 Gly Gly Arg Thr Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr
360          565          570          575
363 Gln Glu Ala Arg Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val
364          580          585          590
367 Thr Ala Glu Arg Leu Val Val His Glu Met Asp Ser Ala His Asn Gln
368          595          600          605
371 Leu Ser Asn Glu Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser
372          610          615          620
375 Arg His
376 625
379 <210> SEQ ID NO: 3
380 <211> LENGTH: 30
381 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/534,861C

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 6,12,13

Seq#:12; Xaa Pos. 5,7,8,11,13